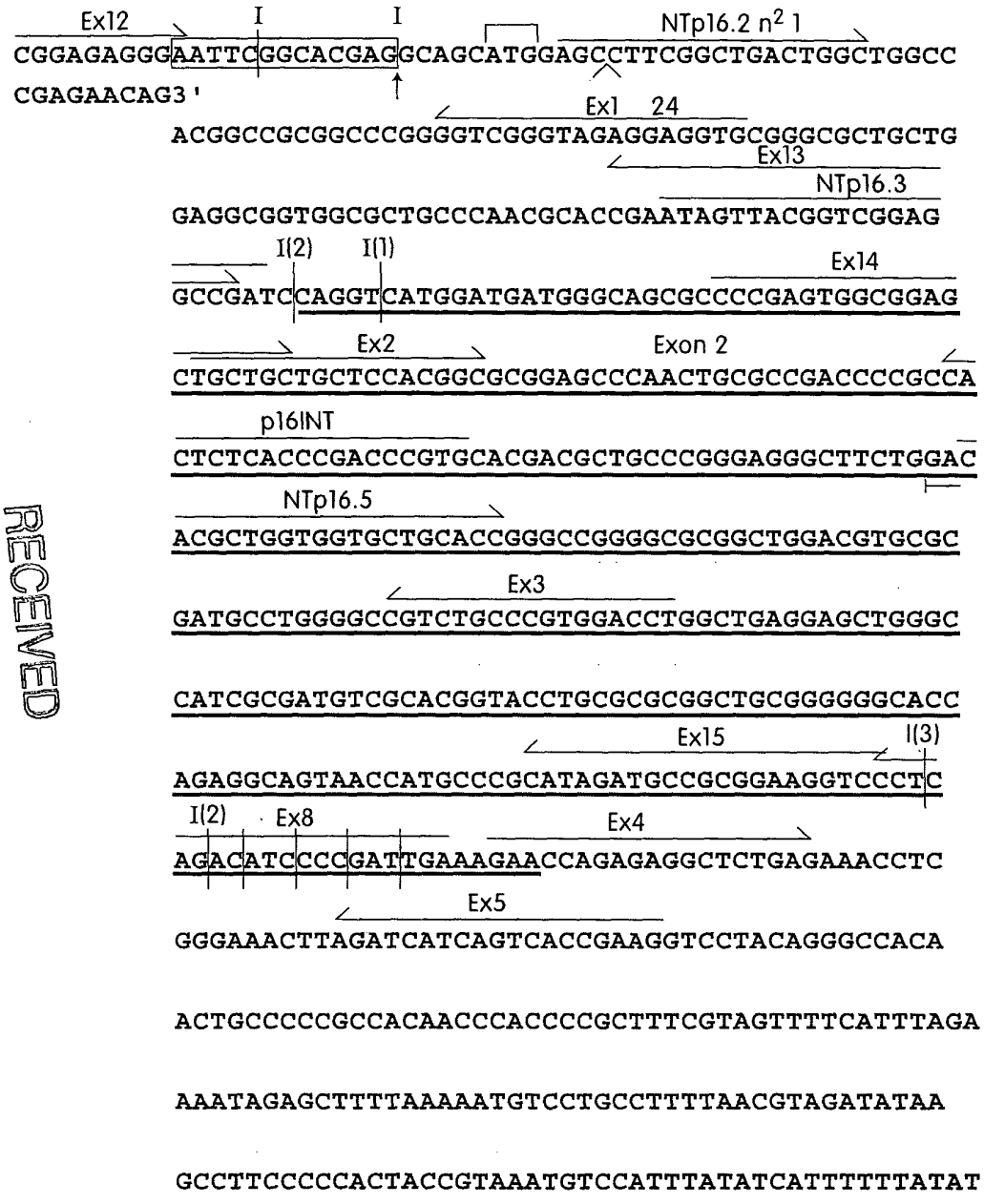


Fig. 1A

ATTCTTATAAAAATGTAAAAAAGAAAAACACCGCTTCTGCCTTT

Ex6

TCACTGTGTTGGAGTTTTCTGGAGTGAGCACTCACGCCCTAAGCG

CACATTCATGTGGGCATTTCTTGCGAGCCTCGCAGCCTCCGGAAG

I I Ex7

CTGTCGACTTCATGACAAGCATTTTGTGAACTAGGGAAGCTCAG

GGGGGTTACTGGCTTCTCTTGAGTCACACTGCTAGCAAATGGCAG

AACCAAAGCTCAAATAAAAATAAAATTATTTTCATTCATTCACT

CAAAAAAA

Fig. 1B

```
p16EX1    < GGNGGNAAGNTGTGGGGGAAAGTTTGGGGATGGAANACCAANCCCTCCTTTCNTTACCAA  60

          .........+.........+.........+.........+.........+.........+

p16EX1    < ACNCTGGCTCTGNCGAGGCTNCNTCCGANTGGTNCCCCCGGGGGGAGACCCAACCTGGGNC  120

          .........+.........+.........+.........+.........+.........+

p16EX1    < GACTTCAGGGNTGCNACATTCACTAAGTGCTNGGAGNTAATANCACCTCCTCCGAGCANx  180
p16EX13   <                      TCNCTTATTGNTAGGANATAATAAcACCtCCACcGAtAACT  41

          .........+.........+.........+.........+.........+.........+

p16EX1    < TCGCTCACAGCGTCCCCTTACCTNGANAGATACCNCGxGxTCCCTCCAGAGGATTTGAGG  240
p16EX13   < TcaCTTACAACGTCCCNNTtCCTGgaAAGATACacaGCGTTCCCTCCAGAGGATTTGTGG  101

          .........+.........+.........+.........+.........+.........+

p16EX1    < GACAGGNTCGGAGGGGGCTCTTCCCCCANCACCGGAGGAAGAAAGAGGAGGGNCTGACTG  300
p16EX13   < GACAGGGTNGGAGNGGTCTCTTCCNCCACCACCGGAGGAAGAAAGAGGAGGGGCTGNCTG  161

          .........+.........+.........+.........+.........+.........+
                                                    Ex1A (12)
p16EX1    < GTCACCAGAGGGTGGGACGGACCGCGTGCGCTCGGCGNCTNCGGAGAGGGGGAGAACAGA  360
p16EX13   < TTCACCAGAGGGTGGGACGGACCNCGTACGCTCGNCGNCTNCGGAGAGGGGGAGAGCAGT  221

          .........+.........+.........+.........+.........+.........+
                                                    I
p16EX1    < CAACGGGCGGCGGGGAGCAGCATGGATCCGGCGGCGGGGAGCAGCATGGANCCTTCGACT  420
p16EX13   < CANCGGNCGNCGGGGAGCAACATGGAACCGNCGGCGGGGAGCAGCATGGANCCTTCGGCT  281

          .........+.........+.........+.........+.........+.........+

P16NT2    <            GACNNNCTCCGGCCGGNGTCGGGTAGAGGAGGTGCGGGCGCTGCTGGAG  49
p16EX1    < GACTGACTGCCTCGC                                               435
p16EX13   < GACTGGCTGNCCACGNCCACGNCCCGGGGTCGGGTAGAGGAGGTGCGGNCGCTNCTGGAG  341

          .........+.........+.........+.........+.........+.........+
                                                              I
P16NT3    >                                Ex13          GTCTNANCCCGGGTA  15
P16NT2    < GCGGGGGCGCTGCCCAACGCACCGAATAGTTACGGTCGGAGGCCGATCCAGGTxxGGGTA  109
p16EX13   < GCGGGGNCTCTGNCCAACNCGCTAAAAN                                  369

          .........+.........+.........+.........+.........+.........+

P16NT3    > GAGGGTCTGCAGCGGGAGCAGNGGATGGCGGGCGACTCTGGAGGACGAAGTTTGCAGGGG  75
P16NT2    < GAGGGTCTGCAGCGGGAGCAGGGGATGGCGGGCGACTCTGGAGGACGAAGTTTGCAGGGG  169

          .........+.........+.........+.........+.........+.........+
                                    Ex1B
P16NT3    > AATTGGAATCAGGTAGCGCTTCGANTCTCCGGAAAAAGGGGAGGCTTCCTGGGGAGTTNN  135
P16NT2    < AATTGGAATCAGGTAGCGCTTCGATTCTCCNGAAAAAGGGGAGGCTTCCTGGGGAGTTTT  229
```

Fig. 2A

```
        .........+.........+.........+.........+.........+.........+

> CAGAAGGGGTTTGTAATCACAGNCCTCCNCCTGGCGACGCCCTGGGGGGTTGGGAAGCCA 195
< CAGAAGGGGTTTGTAATCACAGACCTCCTCCTGGCGACGTCCTGGGGGCTTGGGAAGCCA 289

        .........+.........+.........+.........+.........+.........+

> AGGAAGAGGAATGAGGAGNCACGCGCNTACAGNTCTCTCGAATNCTGANAAGATCTGAAG 255
< AGGAAGAGGAATNAGGAGCCACGCGCGTACAGATCTCTCGAATGCTGAGAAGATCTNAAG 349

        .........+.........+.........+.........+.........+.........+

> GGGGGAACATATTTGTATTAGxATNNAAGTATGCTCTTTATCAGATACAAAATTCACGAA 315
< GGGGGAACATATTTGTATTAGCNTCCAAGTNTNCTCTNTATCANATACAAANTxC      404

        .........+.........+.........+.........+.........+.........+

> CGTGTGGNATAAAAAGGGAGTCTTAAAGAAATNTAAGATGTGCTGGGACTACTTAGCCTC 375

        .........+.........+.........+.........+.........+.........+

> CAANACACAGATNCCTGGATGGAGCT                                    401

        .........+.........+.........+.........+.........+.........+
```

Fig. 2B

```
P16INT   > AAAANNAAAAAAAATCTCCCAGGCCTAACATAATTNTCAGGAAAGAAATTTCAGTAGTTG 60

P16INT   > NATCTCAGGGGAAATACAGGAAGTTAGCCTGGAGTAAAAGTCAGTCTGTCCCTGCCCCTT 120

P16INT   > TGCTANATTGCCCGTGCCTCACAGTGCTCTCTGCCTGTGACGACAGCTCCNCAGAAGTTC 180

P16INT   > GGAGGATATAATGGAATTCATTGTGTACTGAAGAATGGATAGAGAACTCAAGAAGGAAAT 240

P16INT   > TGGAAACTGGAAGCAAATGTAGGGGTAATTAGACACCTGGGGCTTGTGTGGGGGTCTGCT 300
p16EX15  <                                AANAAAAaAgAAATNgAtAANATagAGGAaT 31

                                  Ex2A
P16INT   > TGGCGGTGAGGGGGCTCTACACAAGCTTCCTTTCCGTCATGCCGNCCCCCACCCTGGCTC 360
p16EX15  < gAACANATTAAAAtcAAAAAAGANAACANAgAcaTaATAAAAAAcGAgAATgTTcTAGAG 91

                                  I                          Ex14
P16INT   > TGACCATTCTGTTCTCTCTGGCAGGTCATGATGATGGGCAGCGCCCGAGTGGCGGAGCTG 420
p16EX15  < NTAATcATAATTATAAaggTcAAgACTCATTGATATnAAGGAaATtgAAGGGAAATctTa 151

P16INT   > CTGCTGCTCCACGGCGCGGAGCCCAACTGCTCCGACGCCG                      460
p16EX2   >                          CCTGCNACGACCCCGCCACTCTCACCCGACCCGTG 35
p16EX14  >     NCTCTCACGGTGGGGAGGCCAACTGCGCCGAACCCGCCACTCTCACCCGACCCGCG 56
p16EX15  < acTagCACAANNGNATNAAAAAANAATTcCCACGACACCGCCACTCTCAACCGATCCGTG 211

p16EX2   > CACGACGCTGTCCGGGAGGGTTTCCTGGACACGCTGGTGGTGCTGCACCGGGCCGGGGNG 95
p16EX14  > CACGACGGTGCCCGGGAGGGGTTCCTGGACACGCTGGTGGTGCTGCACCGGGCCGGGGCG 116
p16EX15  < CTCGACACTGCCCGGGAGGTCNTCCTGGACACGCTGGTGGTNCTCCACCGGNCCGGGGCA 271

p16EX2   > CGGTTGGACGTGCGCGATGCCTGGGGCCGCCTNCCCGTGGxACCTGGTTGAGGAGCTGGG 155
p16EX14  > CGGCTGGACGTTCGNGATGCCTGGGGGCNTCTNTCCGTNGxACCTGGCTGAAGAGCTGGN 176
p16EX15  < CGTCTGGACGTGCGCGATGCCTGGGNCCGNCTACCCGTGGTACCTGACTGAGGACCTGGG 331

p16EX2   > NCATCGCGATGTCGCACGGTACCTGCGCGCGGTTGCGGGGGGCACCAGAGGxNAGTNACC 215
p16EX14  > NCATCGNGATGTCGCACGGCCNCTGTGTGNGGNTGCGGGGGGCACCATAGGTCAGTNTCC 236
p16EX15  < CCATCCCGATTTCGCNGGGTANCTGNGNGNGGCTGNGGGGGCCAANAGAGGxCANTACCC 391
```

Fig. 2C

```
p16EX5   < xAAGTATGAGCGAAACNAATTGTGGTTTGAGAANAGGNAATCGTAGGGAACTTCGGGATC 60

         .........+.........+.........+.........+.........+.........+

p16EX5   < CCNCNGGGANCNCCAGAACCTGAGNCGCCNATTGGAAATNACAAACTGNCTGNATCACTC 120

         .........+.........+.........+.........+.........+.........+

p16EX5   < CGNACCAGGTNCAAAAGATACCTGGGGANGCGGGAAGGGAAAGACNACATCNAGACCGCC 180
p16EX9   <                                                        CCCC 4

         .........+.........+.........+.........+.........+.........+

p16EX5   < TTCGCNCCTXGGNATTGTGAGCAGCCTCTGAGACTCATTXATATNACACTCGTXTTTCTT 240
p16EX9   < ATCGCGCCTTGGGANTGTGAGCNACCATTGAGACTCATNAATATAGCACTCGTTTTTCTT 64

         .........+.........+.........+.........+.........+.........+

p16EX5   < CTTACAACCCTGCGGNCCGCGCGGTCGCGCTTTCTCTGCCCTCCGCCGGGTGGACCTGGA 300
p16EX9   < CTTGCAACCCTGCGGNCCGCGCGGTCGCGCTNTCTCTGCCCTCCGCNGGGTGGACCTGGA 124

         .........+.........+.........+.........+.........+.........+

p16EX5   < GCGCTTGAGCGGTCGGCGCGCCTGGAGCAGCCAGGCGGNCAGTGGACTAGCTGCTGGACC 360
p16EX9   < GCGCTTGAGCGGTCGGCGCNCCTGGANCAGCCAGGCGGGCAGTGGACTACCTNCTGGACC 184

         .........+.........+.........+.........+.........+.........+

p16EX5   < AGGGAGGTGTGGGAGAGCGGTGGCGGCGGGTACATGCACGTGAAGCCATTGCGAGAACTT 420
p16EX9   < AGGGAGGTGTGGGAGAGCGGTGNCGGCGGGTACATGCACGTGAAGCCATTGCGAGAACTT 244

         .........+.........+.........+.........+.........+.........+

p16EX5   < TATCCATAAGTATTTCAATACCGGTAGGGACGGCAAGAGAGGAGGGCGGGATGTGCCACA 480
p16EX9   < TATCCATAAGTATTTCAATGCCGGTAGGGACGGCAAGAGAGGAGGGCGGGATGTNCCACA 304

         .........+.........+.........+.........+.........+.........+
                                                          I
p16EX5   < CATCTTTGACCTCAGGTTTCTAACGCCTGTTTTCTTTCTGCCCTCTGCAGACAACCCCGA 540
p16EX9   < CATCTTTGACCTCAGGTTTCTAACGCCTGTTTTCTTTCTGCCCTCTGCAGACATCCCCGA 364

         .........+.........+.........+.........+.........+.........+

p16EX4   >                                    AGAAATTAGATCATCAGTCACCGATG 26
p16EX5   < TTGAAAGAACCAGAGAGGCTCTGAGAAACC                               570
p16EX9   < TTGAAAGAACCAGAGAGGCTCTGAGAAACCTCCGGAAACTTAGxTCATCAxTCGCCGNAA 424

         .........+.........+.........+.........+.........+.........+

p16EX4   > GTCCTACAGGGNCACAACTGNCCCCGCCACAACCCACCCCGNTTTCGTAGTTTTCATTTA 86
p16EX9   < AA                                                          426

         .........+.........+.........+.........+.........+.........+
```

Fig. 3A

```
p16EX4   > GAAAATAGAGCTTTTAAAAATGTCCTGCCTTTTAACGTAGATATATGCCTTCCCCCACTA 146

           .........+.........+.........+.........+.........+.........+

p16EX4   > CCGNAAATGTCCATTTATATCATNTTTTATATATTCTTATAAAAATGTAAAAAAGAAAAA 206

           .........+.........+.........+.........+.........+.........+

p16EX4   > CACCGCTTCTGCCTTTTCACTGTGTTGGAGTTTTCTGGAGTGAGCACTCACGCCCTAAGC 266

           .........+.........+.........+.........+.........+.........+

p16EX6   >   CANCNATNTNCGGCATTTCTNGNGAGCCTCGTAGTCTCCGGATGNTGTCGACCTCGAG 58
p16EX6a  >   CANCNATNTNCGGCATTTCTNGNGAGCCTCGTAGTCTCCGGATGNTGTCGACCTCGAG 58
p16EX4   > GCACATTCATGTGGGCATTTCTTGCGAGCCTCGCAGNCTCCGGAAGCTGTCGACCTCGAG 326

           .........+.........+.........+.........+.........+.........+

p16EX6   > GGGGGGNCCNGTACCCAATTCGNCCTATNGTGAGTCGTNTTACAATTCACTGGCCGCCGT 118
p16EX6a  > GGGGGGNCCNGTACCCAATTCGNCCTATNGTGAGTCGTNTTACAATTCACTGGCCGCCGT 118
p16EX4   > GGGGGGNCCGGTACCCAATTCGCCCTATAGTGAGTCGTATTACAATTCACTGGNCGNCGN 386

           .........+.........+.........+.........+.........+.........+

p16EX6   > TTTxACAACGTCGxTGxACTGGGAAAACCCTGGTGTTACCCAACTTxAATCGCCTTGNAG 178
p16EX6a  > TTTxACAACGTCGxTGxACTGGGAAAACCCTGGTGTTACCCAACTTxAATCGCCTTGNAG 178
p16EX4   > TTTTACAACGTCGGTGGACTGGGAAAACCCCGGNGTTACCCAACTTTAATCGNCTTGGAG 446

           .........+.........+.........+.........+.........+.........+

p16EX6   > NACATCCCCCTTTxCGCCAGCTGGTGTAATAGCGANGAGGCCCGCACCGATCGCCCTTCC 238
p16EX6a  > NACATCCCCCTTTxCGCCAGCTGGTGTAATAGCGANGAGGCCCGCACCGATCGCCCTTCC 238
p16EX4   > GACATCCCCCTTTTCGCCAGNTGGGGTTATAGNGAAGAGGGCCNCACCNNTCGCCC     502

           .........+.........+.........+.........+.........+.........+

p16EX6   > CAACAGTTGNGCAGCCTGAATGGCGAATGGAAATTGTAAGCGTTAATATTTTGTTAAAAT 298
p16EX6a  > CAACAGTTGNGCAGCCTGAATGGCGAATGGAAATTGTAAGCGTTAATATTTTGTTAAAAT 298

           .........+.........+.........+.........+.........+.........+

p16EX6   > TCGCGTTANATCNTCGGTTAANTCAGCTCATNTTTTATCCAATAGGCCGANATCGGCANA 358
p16EX6a  > TCGCGTTANATCNTCGGTTAANTCAGCTCATNTTTTATCCAATAGGCCGANATCGGCANA 358

           .........+.........+.........+.........+.........+.........+

p16EX6   > ATCCCCAATAAATCAANAGAATAGACCGAGATAGGGTTGAGTGTCGTTCCAGTTNGGGAA 418
p16EX6a  > ATCCCCAATAAATCAANAGAATAGACCGAGATAGGGTTGAGTGTCGTTCCAGTTNGGGAA 418

           .........+.........+.........+.........+.........+.........+

p16EX6   > CANGAGTCCACTATTAAAGANCGTAGNCTCNAACGTCANAGGGCGAAAAACCNTNTTTCA 478
p16EX6a  > CANGAGTCCACTATTAAAGANCGTAGNCTCNAACGTCANAGGGCGAAAAACCNTNTTTCA 478

           .........+.........+.........+.........+.........+.........+
```

Fig. 3B

```
p16EX6     > GNGGATTGGNCCACTACGCNTANCC                                  503
p16EX6a    > GNGGATTGGNCCACTACGCNTANCCATCACCCTATTC                      515
             .........+.........+.........+.........+.........+.........+
```

Fig. 3C

H9	U18	CCL119	MCF-7	HTB 125	SaOs2	A431	NORMAL #1	NORMAL #2	CELL
ABSENT	ABSENT	ABSENT	ABSENT	ABSENT	ALTERED	ALTERED	NORM	NORM	EXON 1
ABSENT	ABSENT	ABSENT	ABSENT	ABSENT	ALTERED	ABSENT	NORM	NORM	EXON 2

WI38	CCL120	HeLa	HTB100	ZRB75	GM130	Tera2	HTB172	HTB173	CELL
NORM	NORM	NORM	NORM	NORM	NORM	NORM	NORM	NORM	EXON 1
NORM	NORM	NORM	NORM	NORM	NORM	NORM	NORM	NORM	EXON 2

Fig. 4

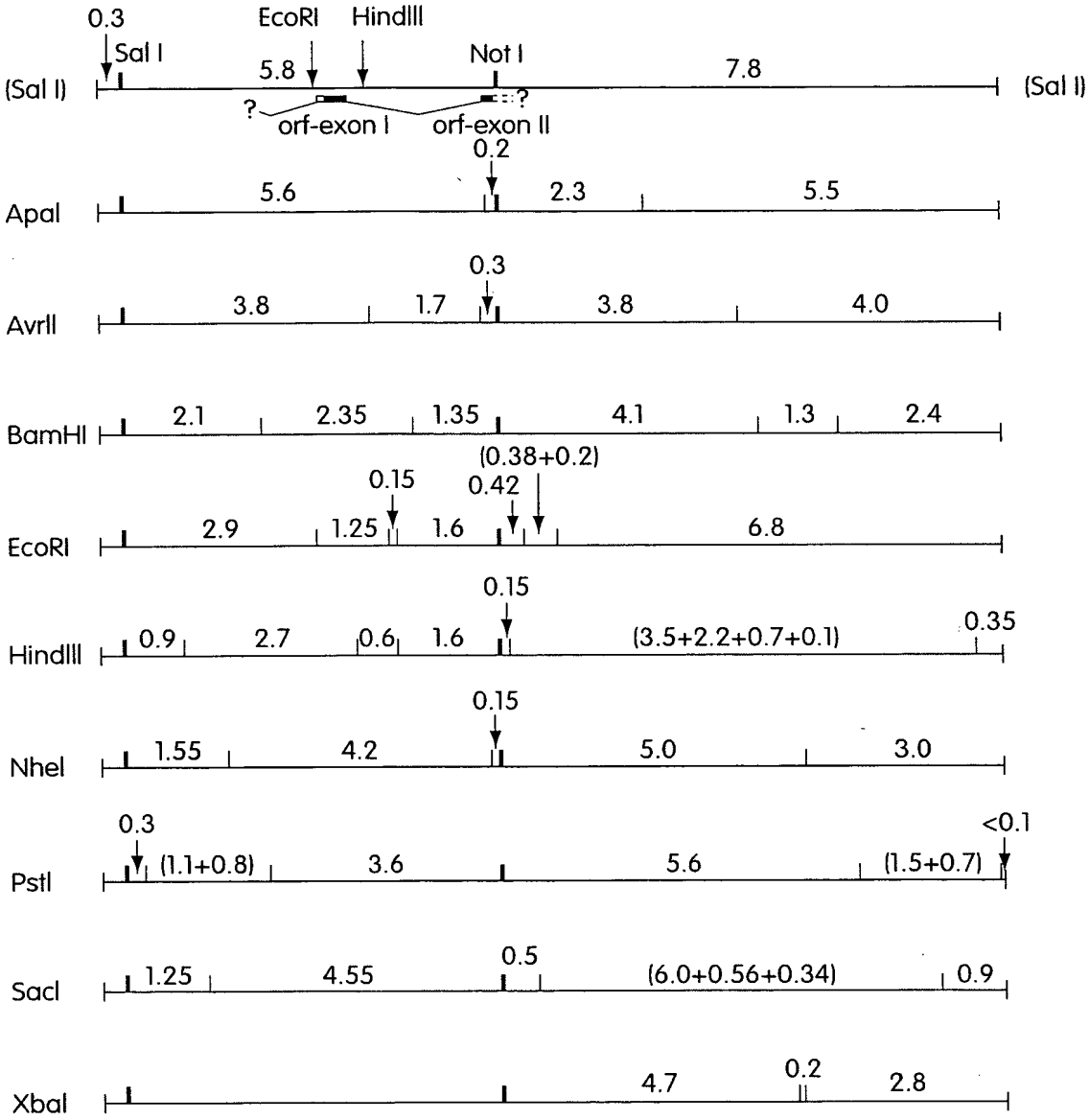
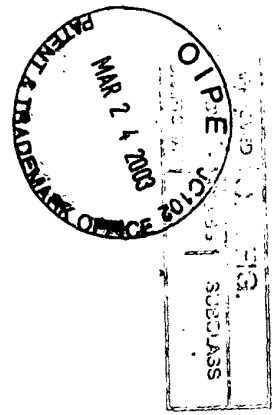


Fig. 5




```
p16:  Ile Gln Val Met Met Met Gly Ser Ala Arg Val Ala Glu Leu Leu Leu Leu His Gly Ala Glu Pro Asn Cys Ala Asp Pro Ala
p15:  Ile Gln Val Met Met Met Gly Ser Ala Arg Val Ala Glu Leu Leu Leu Leu His Gly Ala Glu Pro Asn Cys Ala Asp Pro Ala
p13:              Met Met Met Gly Asn Val His Val Ala Ala Leu Leu Leu Asn Tyr Gly Ala Asp Ser Asn Cys Glu Asp Pro  *

      Thr Leu  *  Thr Arg Pro Val His Asp Ala Ala Arg Glu Gly Phe Leu Asp Thr Leu Val Val Leu His Arg Ala Gly Ala Arg
      Thr Leu  *  Thr Arg Pro Val His Asp Ala Ala Arg Glu Gly Phe Leu Asp Thr Leu Val Val Leu His Arg Ala Gly Ala Arg
      Thr Thr Phe Ser Arg Pro Val His Asp Ala Ala Arg Glu Gly Phe Leu Asp Thr Leu Val Val Leu His Gly Ser Gly Ala Arg

      Leu Asp Val Arg Asp Ala Trp Gly Arg Leu Pro Val Asp Leu Ala Glu Glu Leu Gly His Arg Asp Val Ala Arg Tyr Leu Arg
      Leu Asp Val Arg Asp Ala Trp Gly Arg Leu Pro Val Asp Leu Ala Glu Glu Arg Gly His Arg Asp Val Ala Gly Tyr Leu Arg
      Leu Asp Val Arg Asp Ala Trp Gly Arg Leu Pro Leu Asp Leu Ala Gln Glu Arg Gly His Gln Asp Ile Val Arg Tyr Leu Arg

      Ala Ala Ala Gly Gly Thr ....
      Thr Ala Thr Gly Asp
      Ser Ala  *  Gly Cys Ser ....
```


Fig. 6